

Figure 1

Glucose growth, long-term starvation, and multiplexed data acquisition

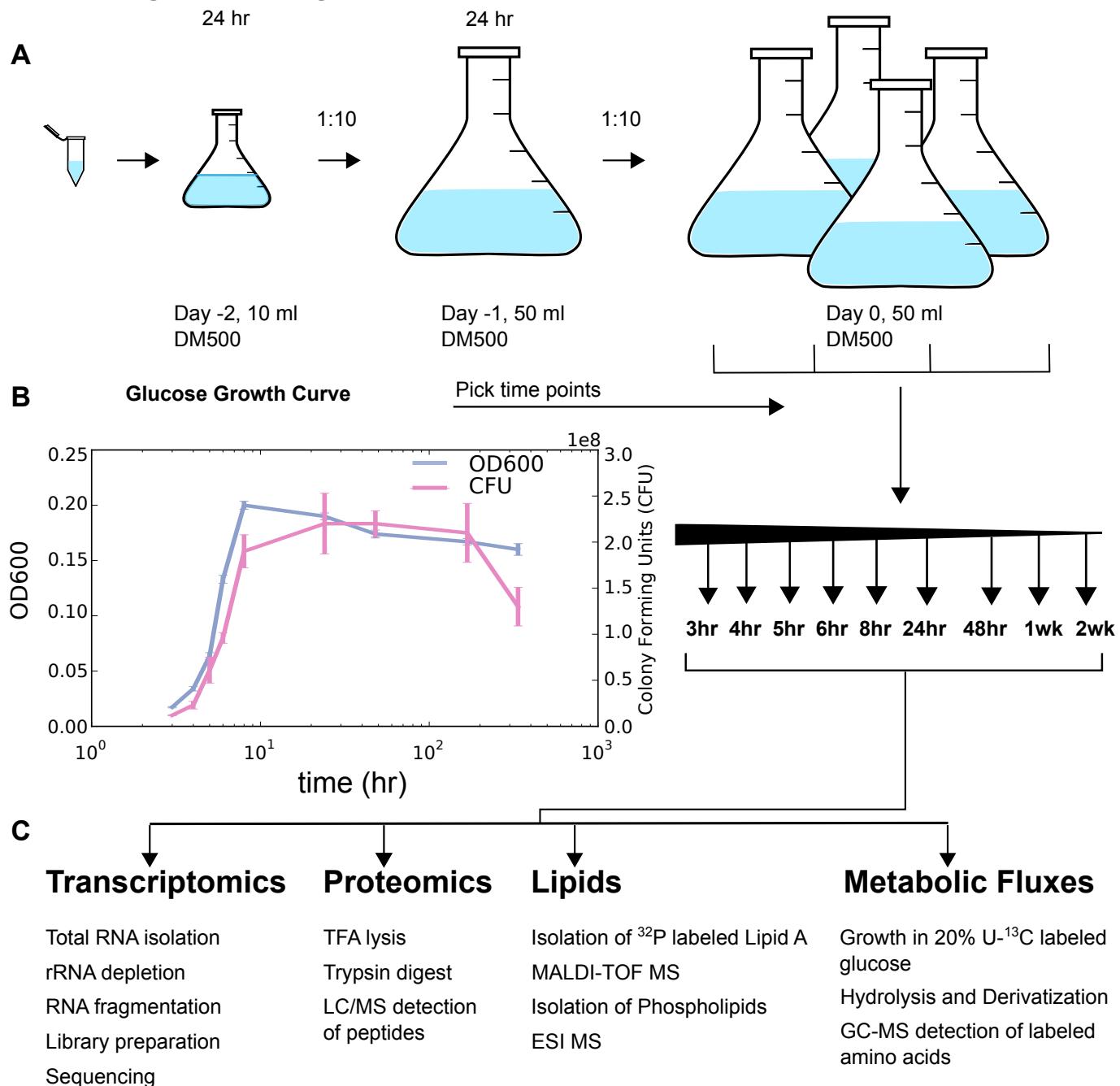


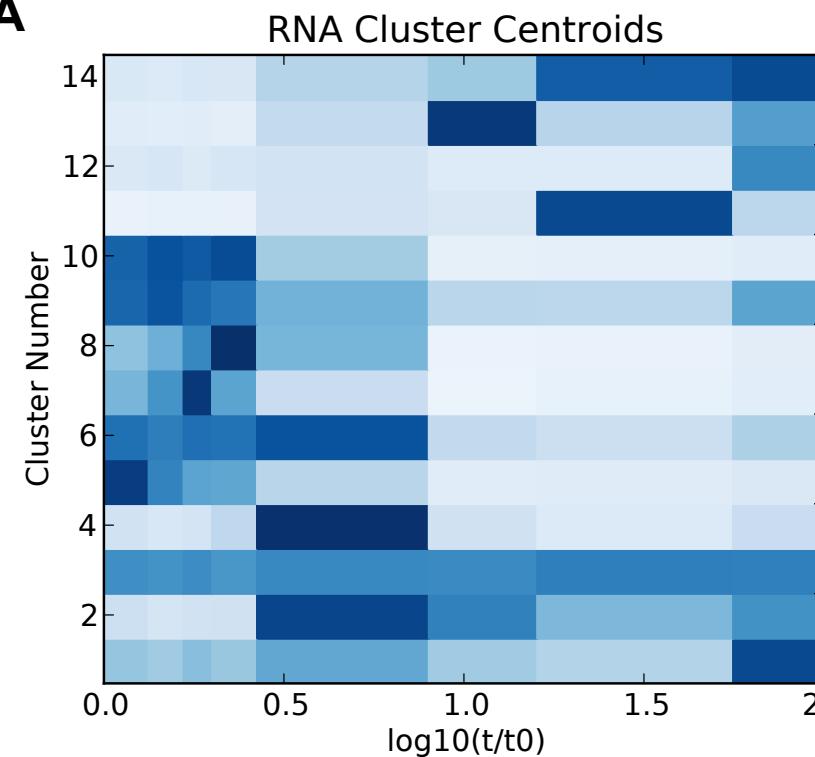
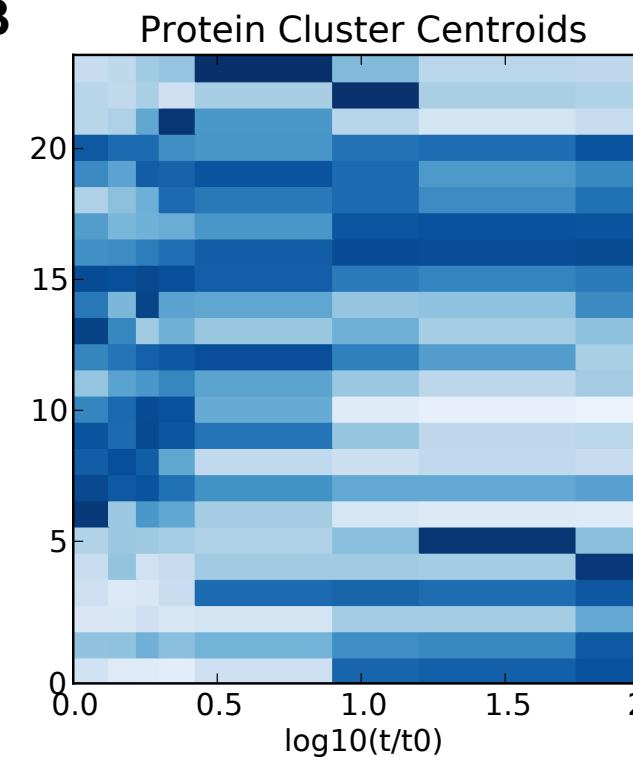
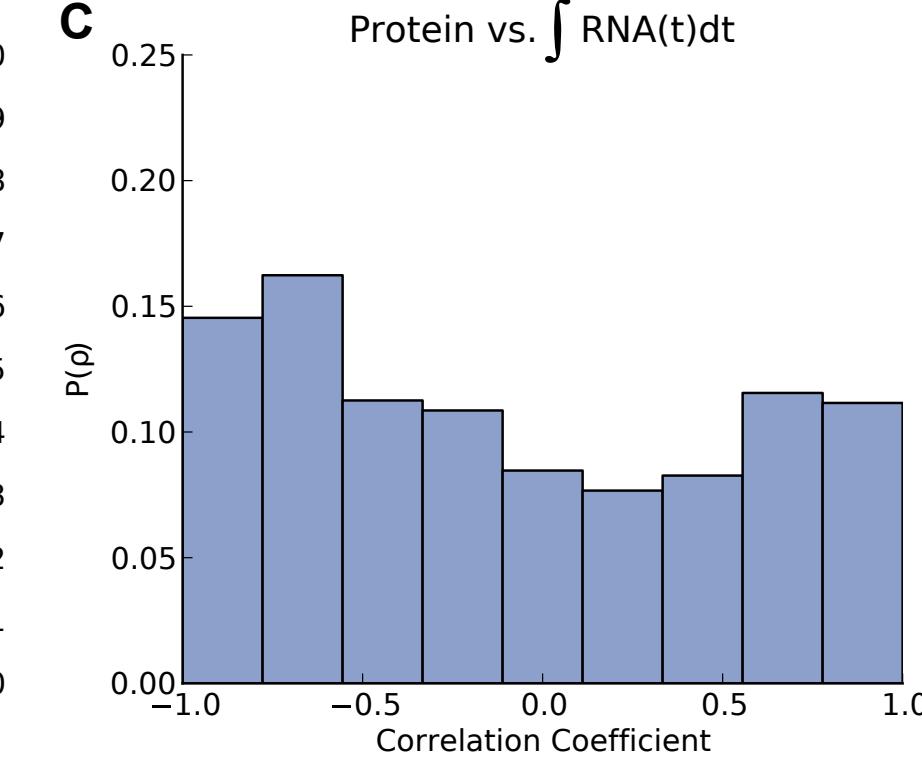
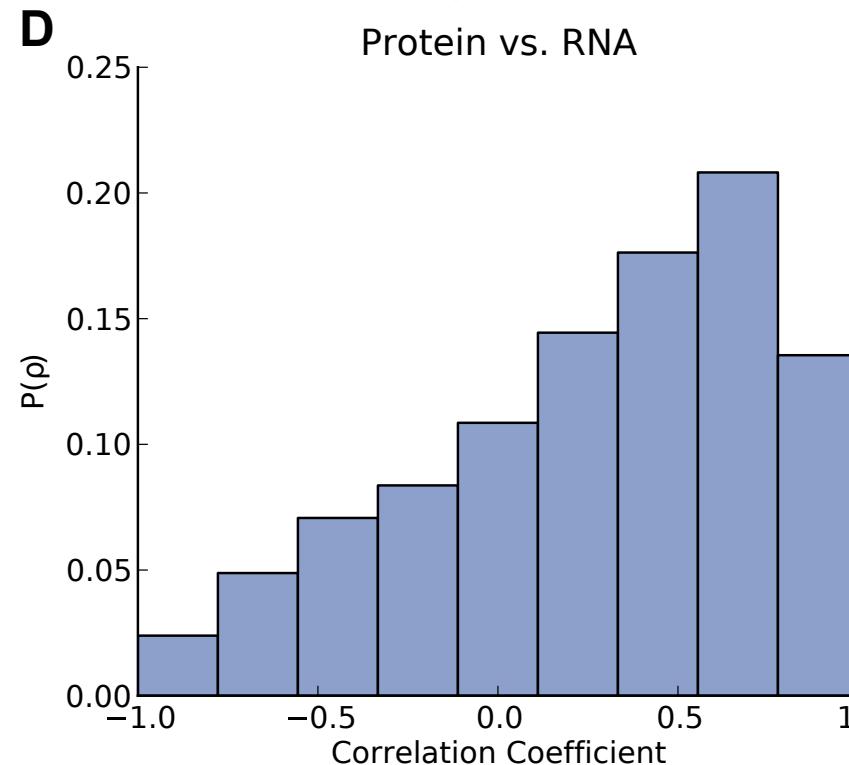
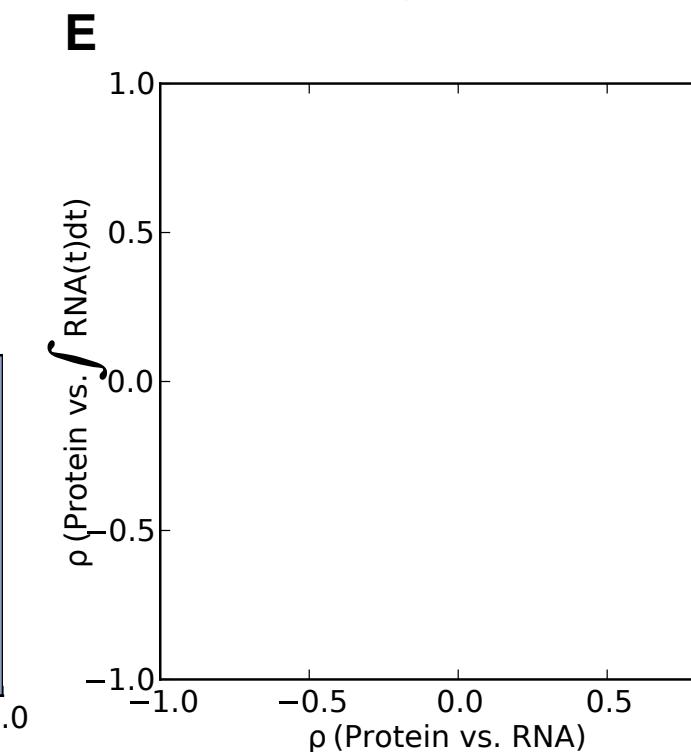
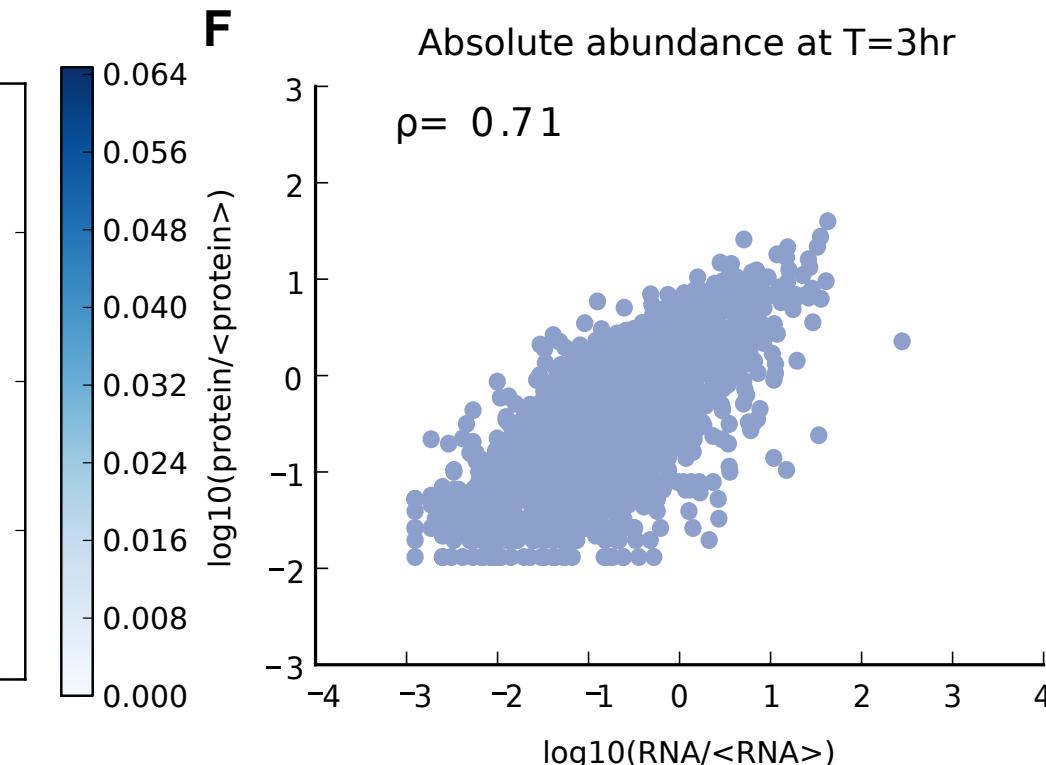
Figure 2**A****B****C****D****E****F**

Figure 3

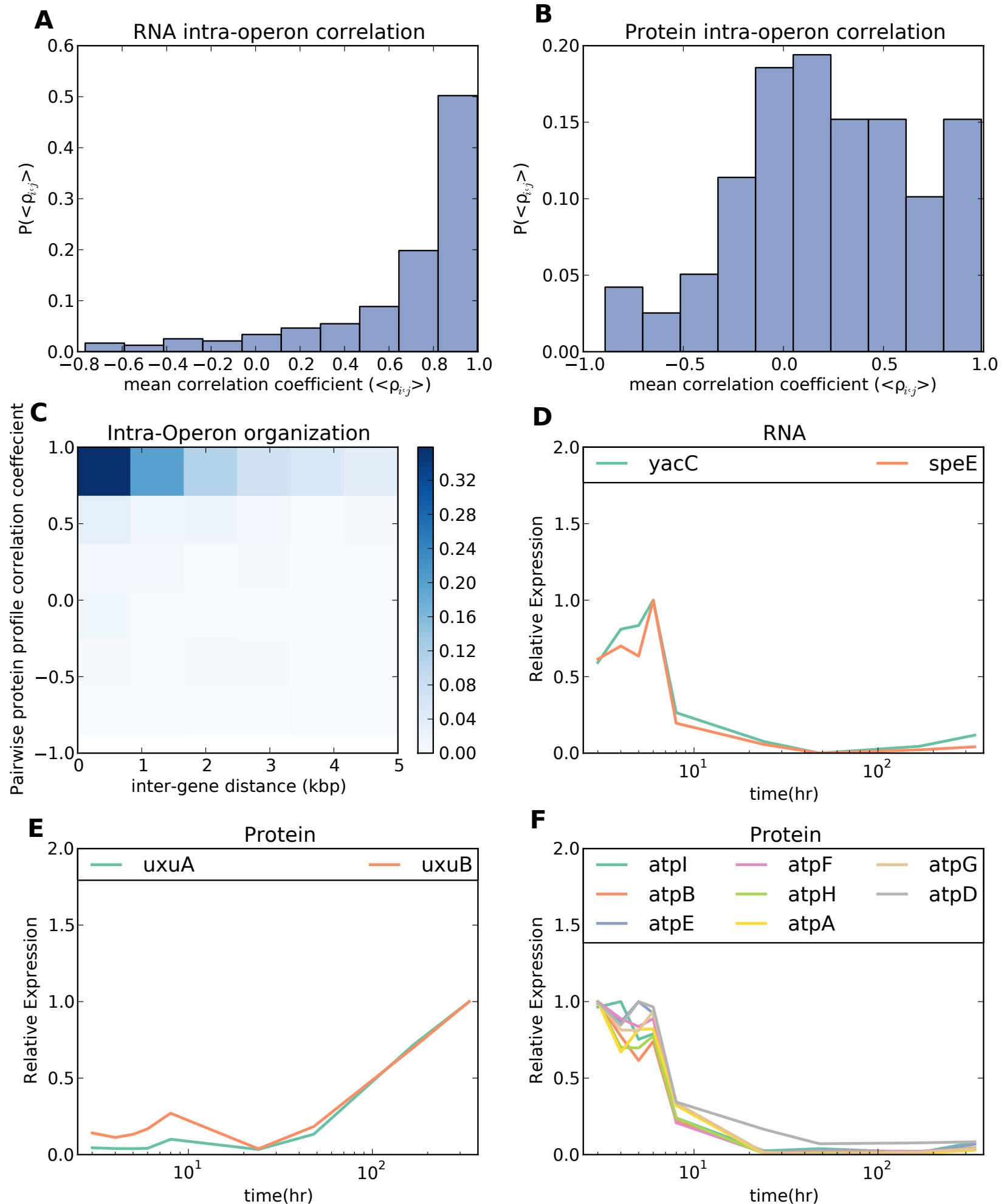


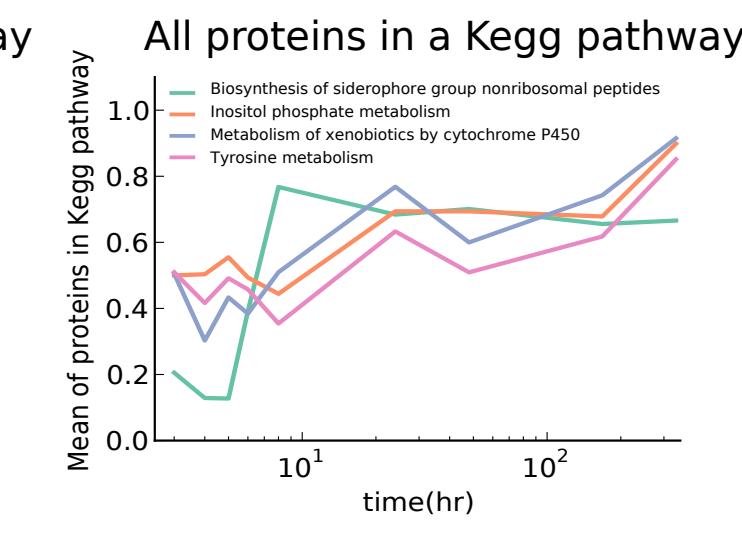
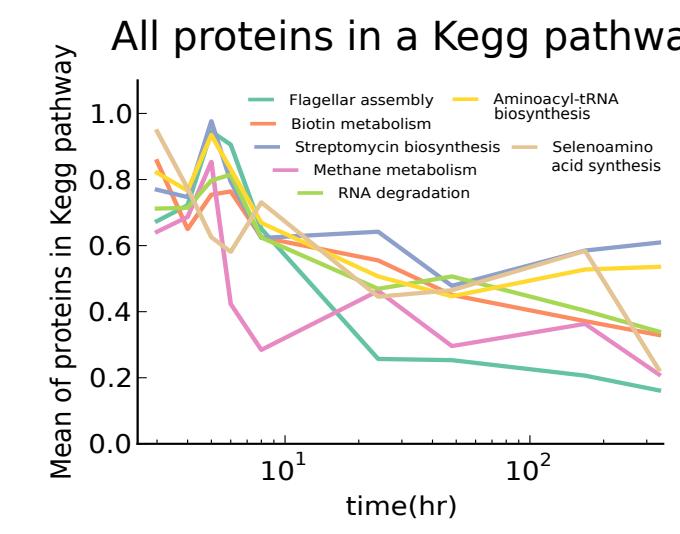
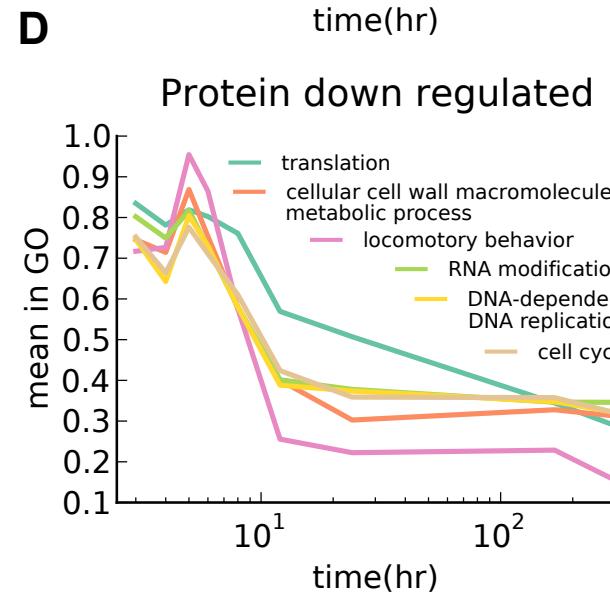
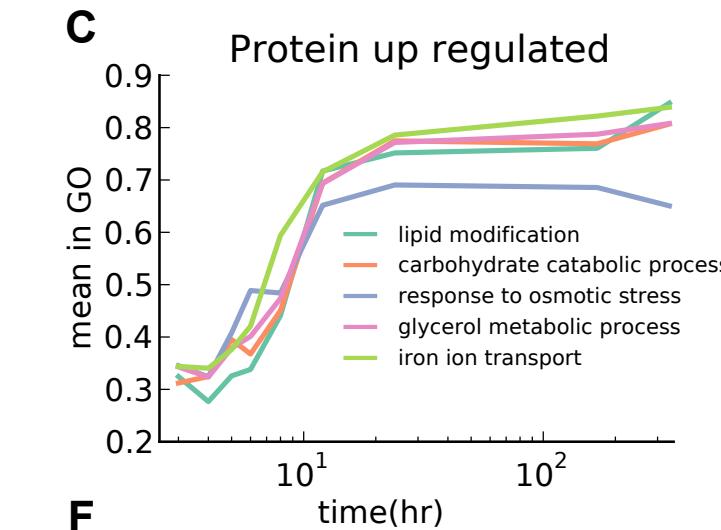
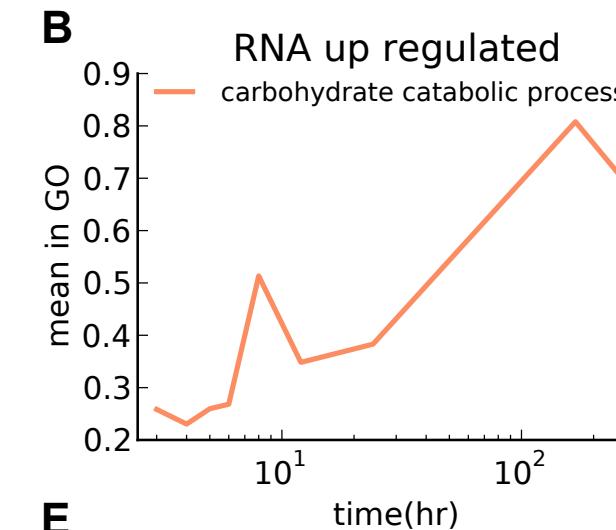
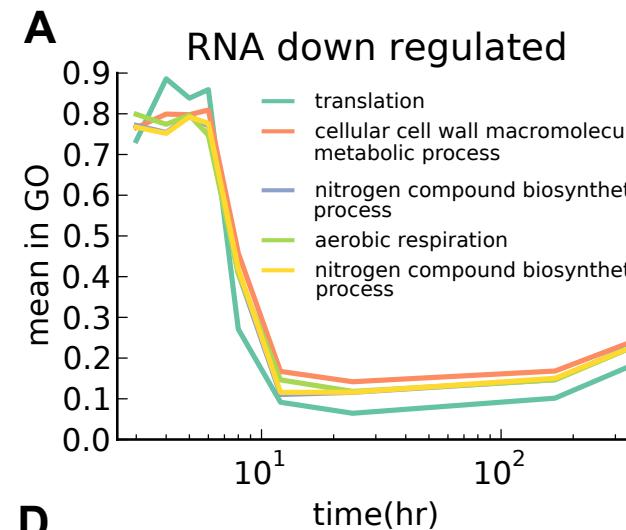
Figure 4

Figure 5

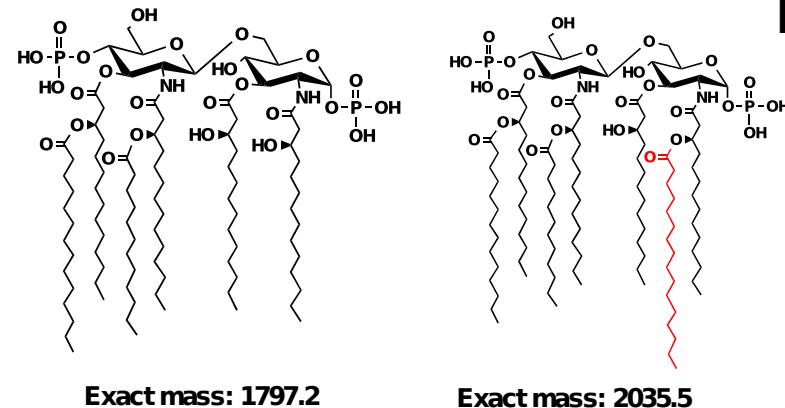
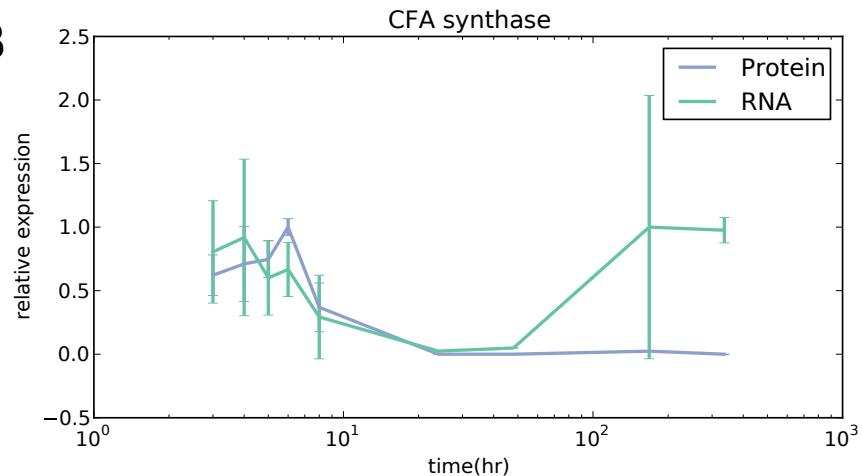
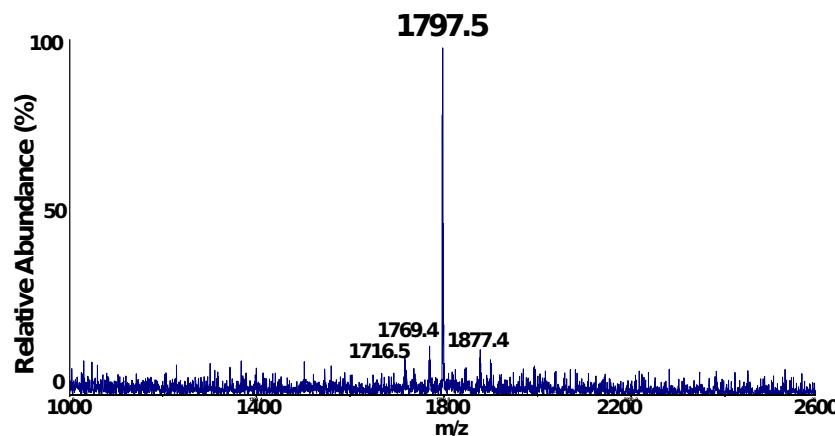
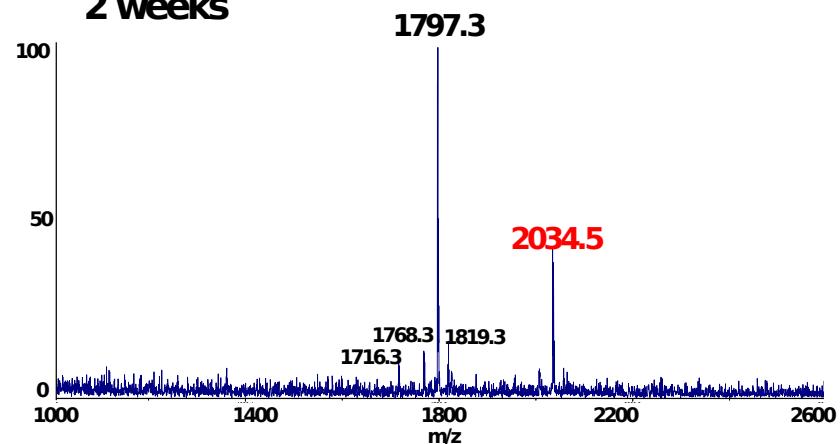
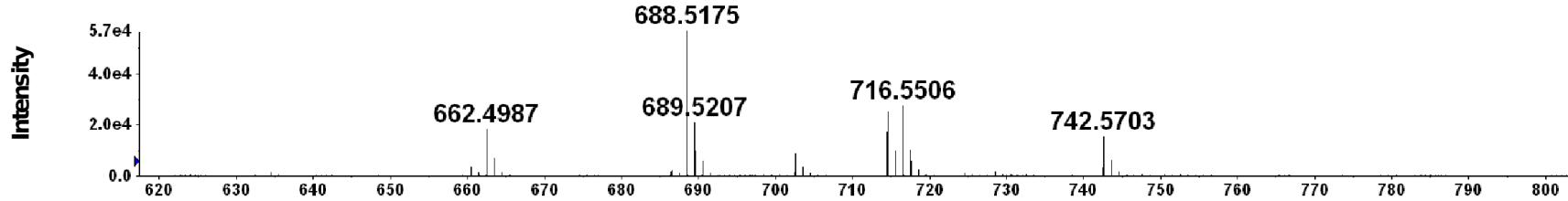
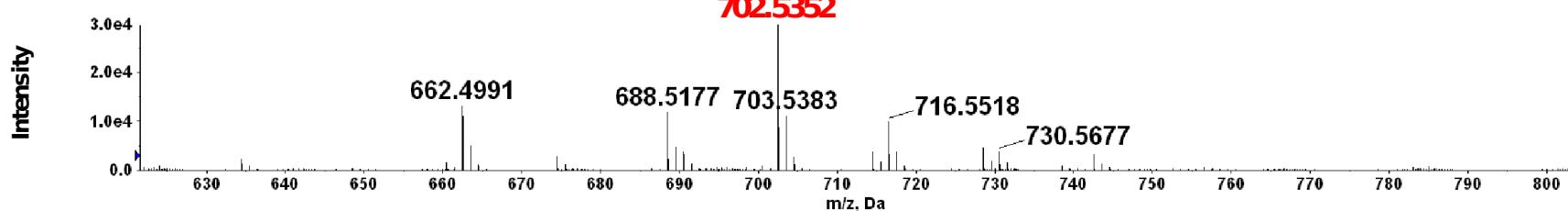
A**B****C****2 weeks****D 6 hours****2 weeks**

Figure 6

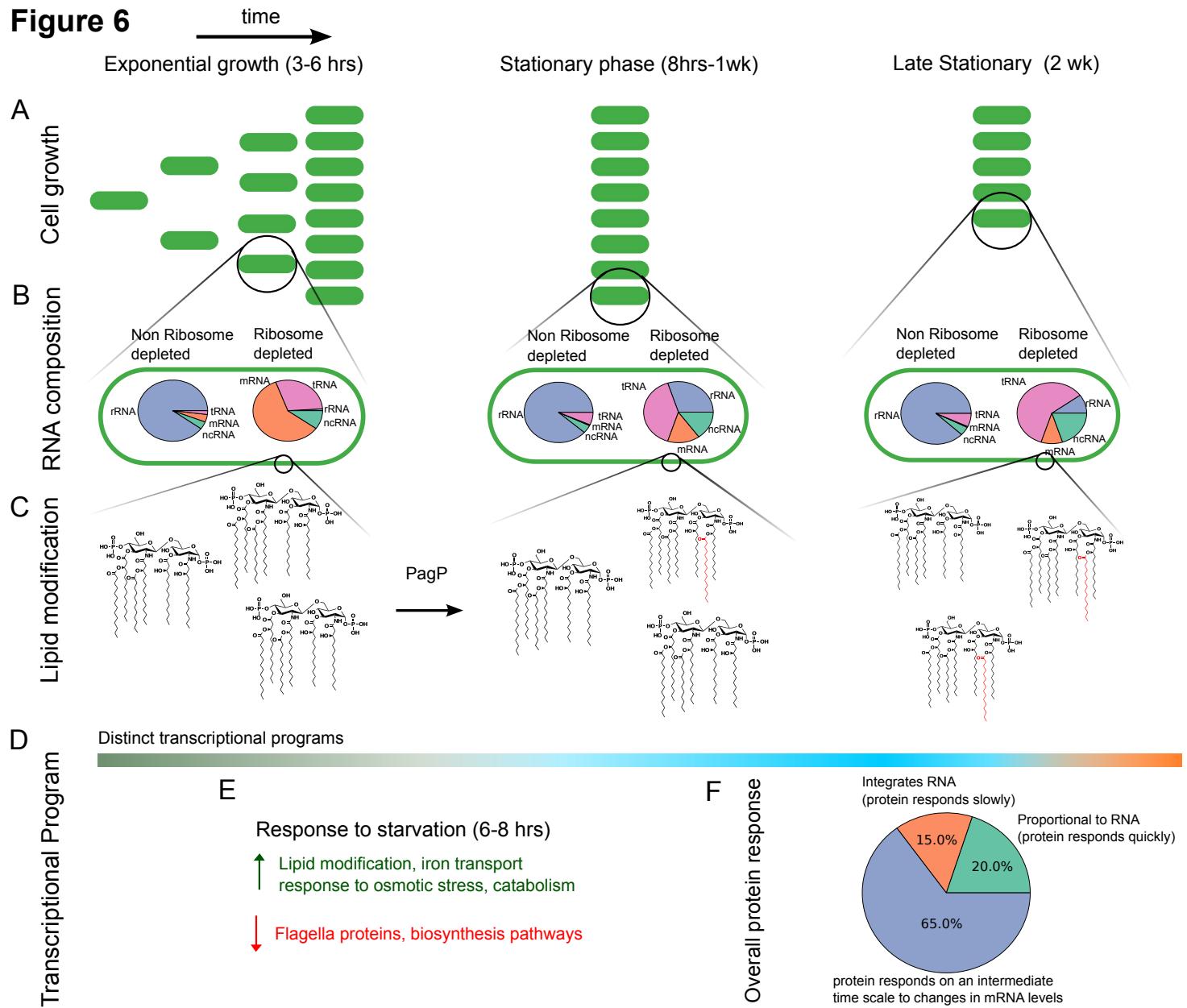


Table 1

Publication	N proteins found	Cutoff	Method	#RNAs	Cutoff	Method
This study	2648 * (at 3hrs)	FDR<1%	Shotgun MS	4116 genes, 89 sRNA, 85 tRNA (at 3hrs)	Alignment quality>10	RNA-seq
Yoon et al. 2012	60	fold change>2	2-D gel	4144 gene probes (REL606 strain)	NA	Microarray
Taniguchi et al.i 2012	1018	NA	YFP fusion	137	95% confidence	FISH
Lewis et al. 2010	~1,000	P-value<0.05	Shotgun MS			
Lewis et al. 2009				4428 gene probes	NA	Microarray
Soares et al. 2013	2053*	FDR<1%	SILAC			
Wisniewski and Rakus, 2014	2200	FDR<1%	FASP			
Raghavan et al. 2011				Genes: 4161, 133 sRNA	%region mapped ≥50%	RNA-seq

*The criteria that Soares et al. use for a protein being observed is that it appear in at least 1 of 2 biological repeats. We use a criteria that it appear in 1 of 3 biological repeats.

Figure E1

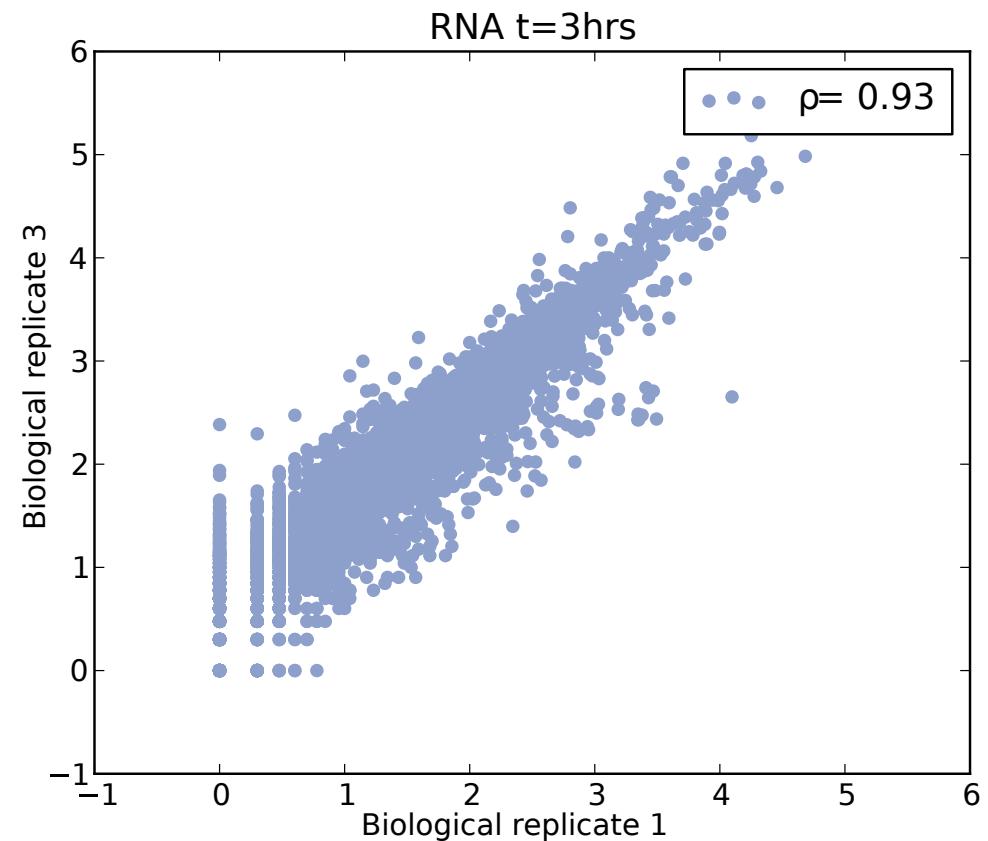
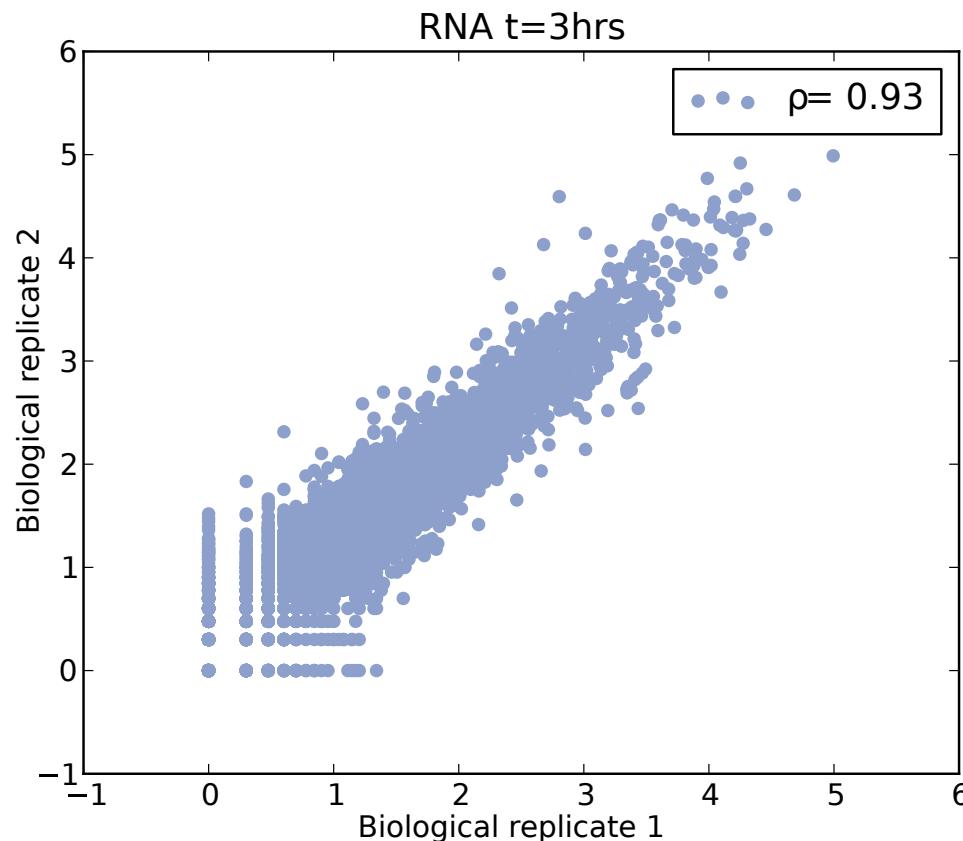
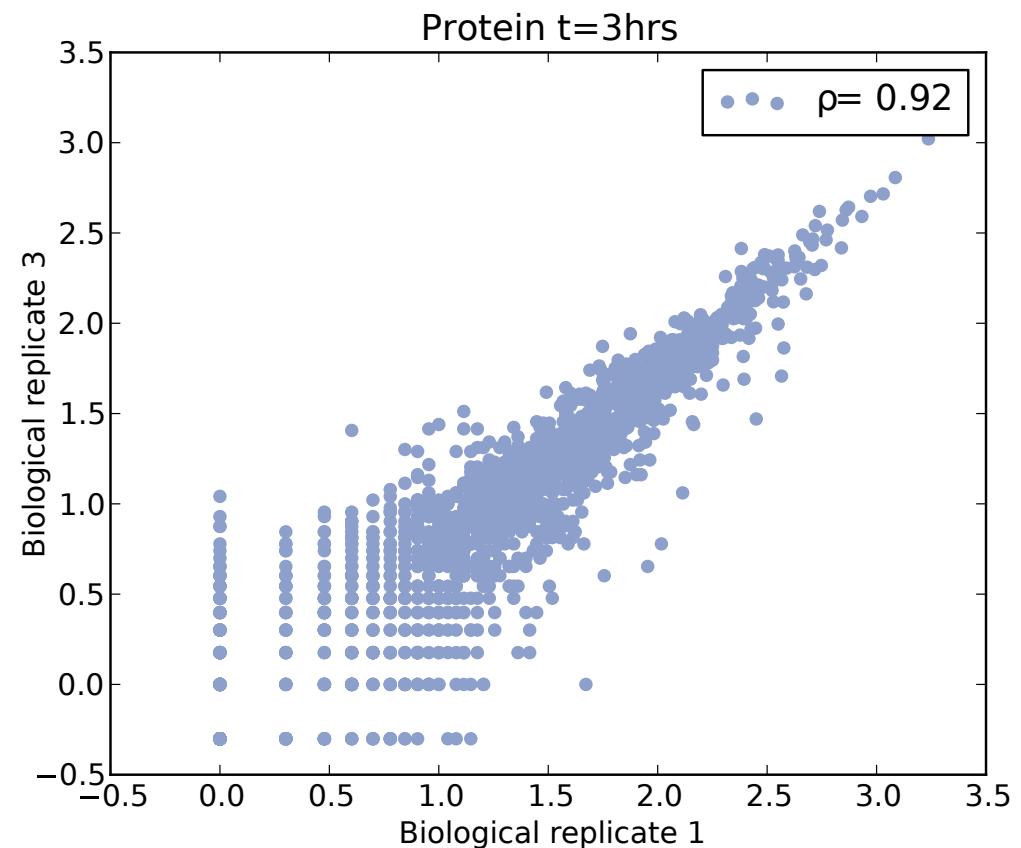
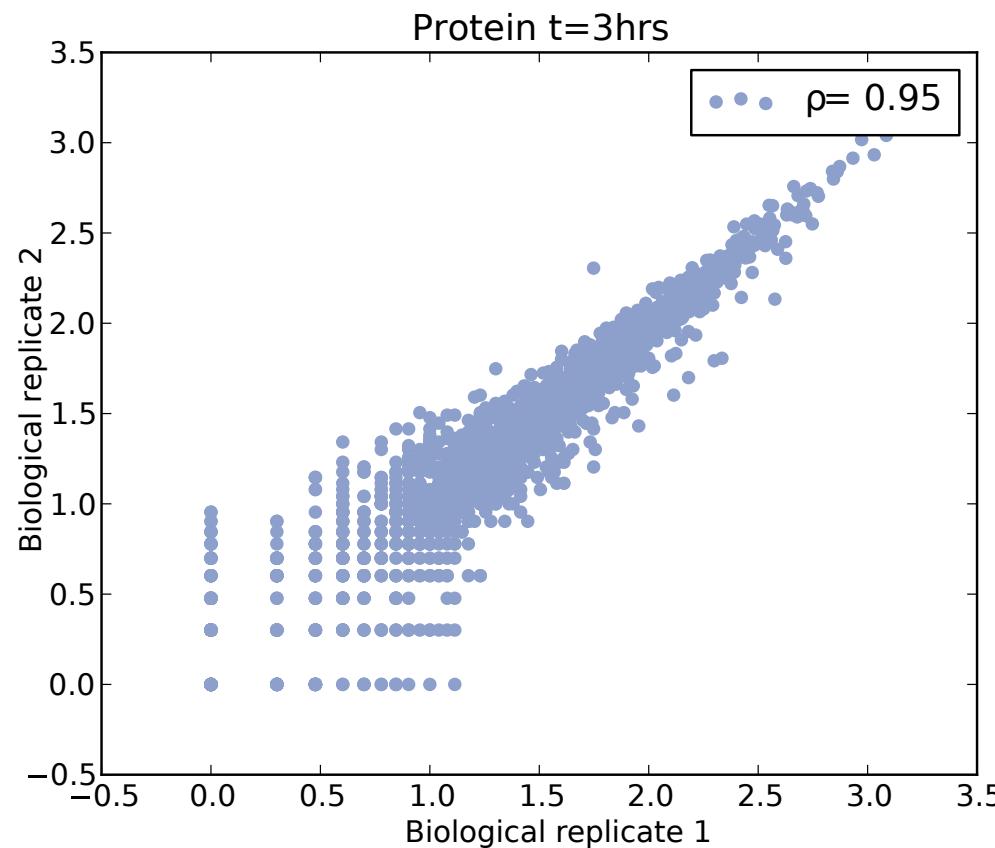


Figure E2

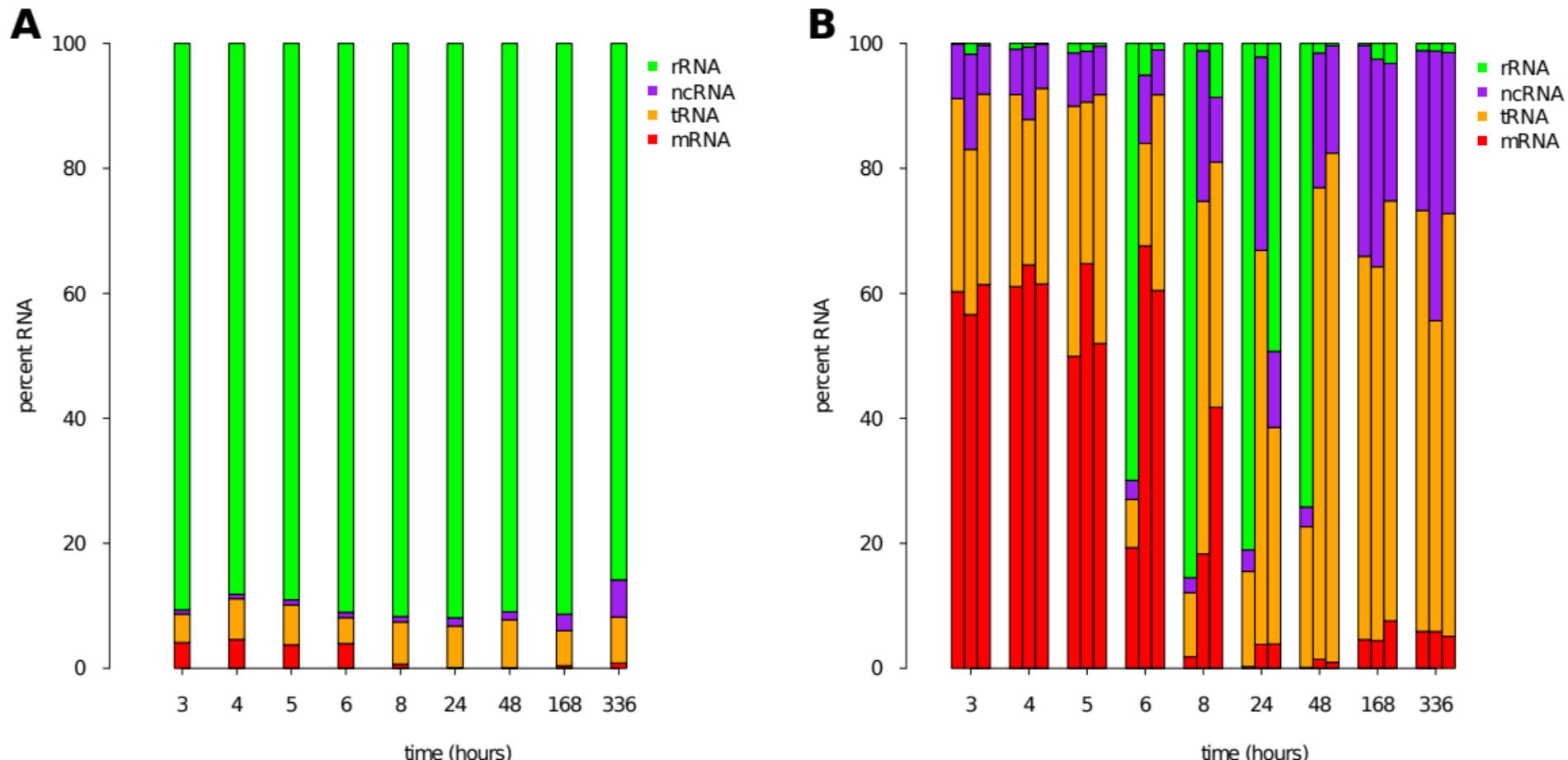


Figure E3

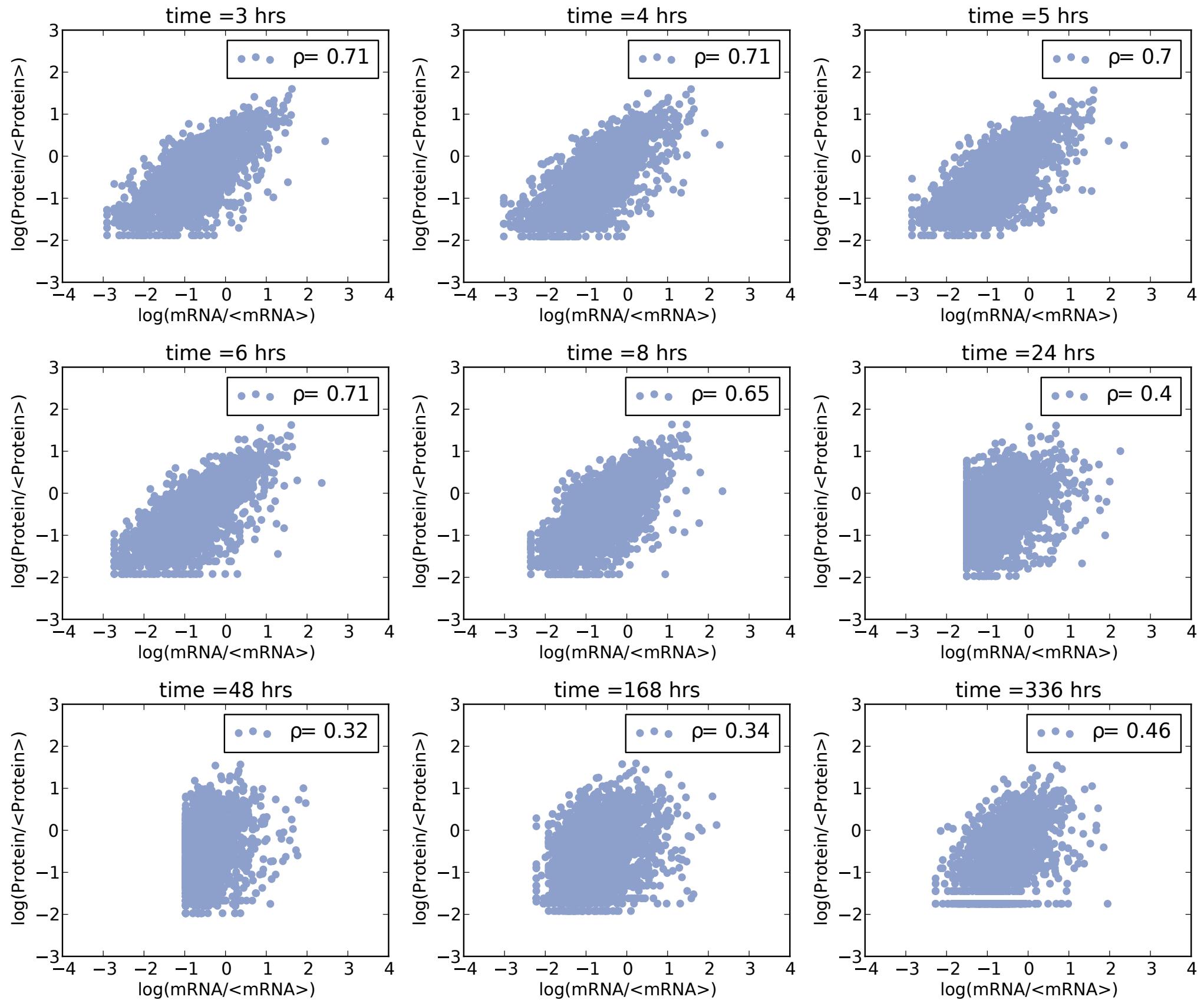


Figure E4

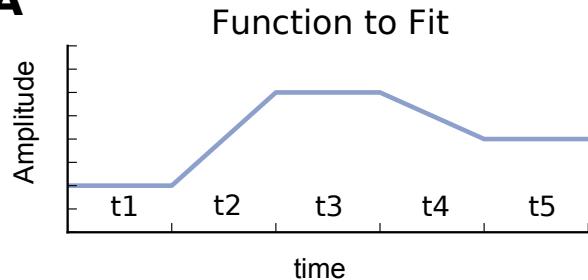
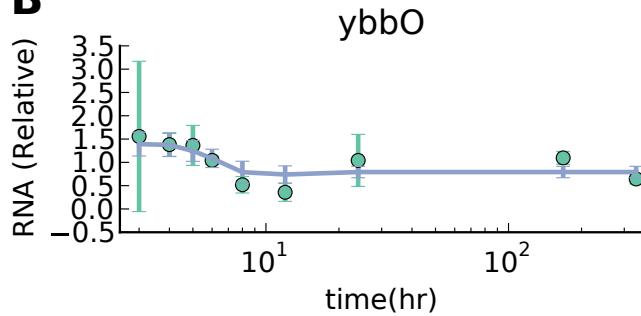
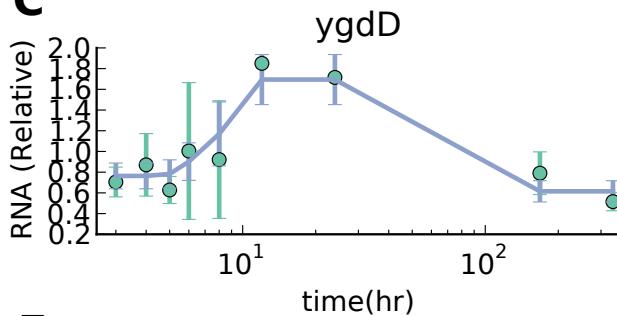
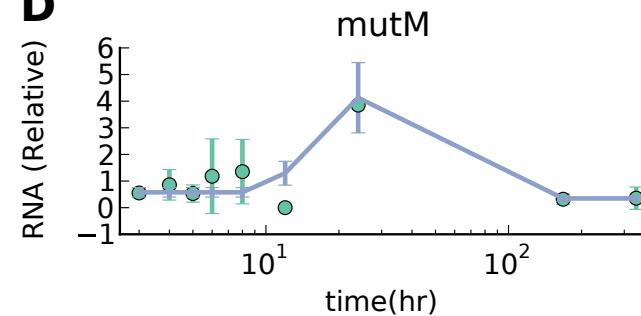
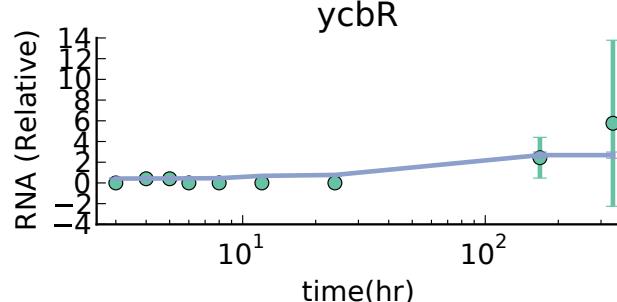
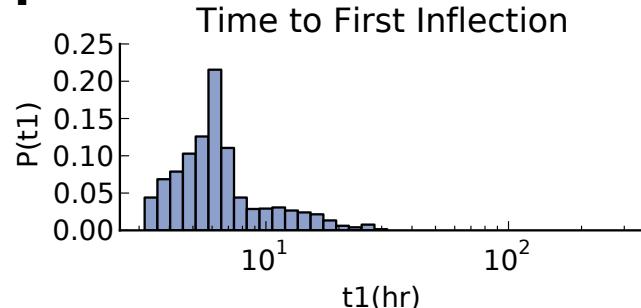
A**B****C****D****E****F**

Figure E5

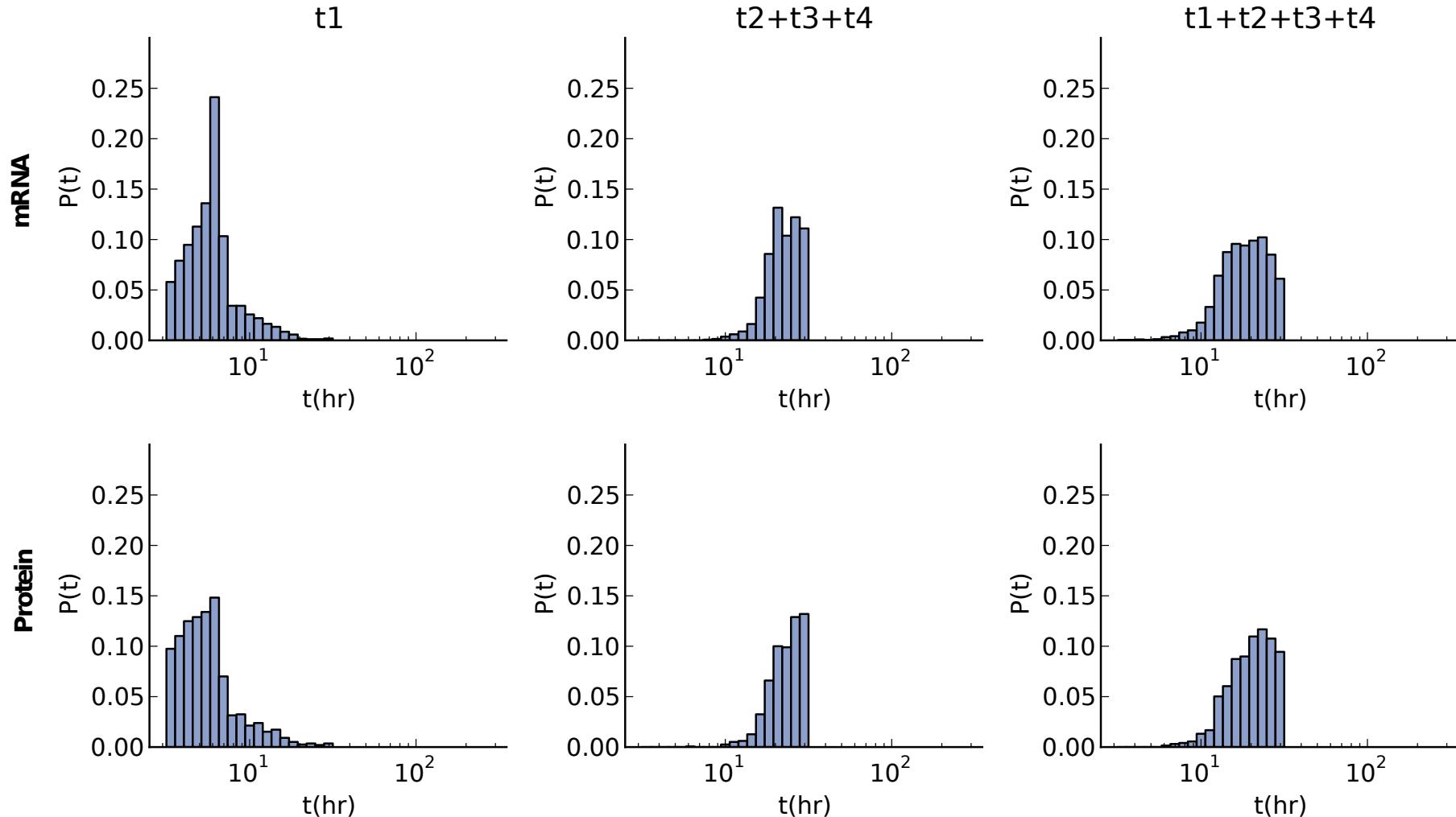


Figure E6

